1

SEQUENCE LISTING

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<130> 1017PC1

<160> 77

<170> PatentIn version 3.1

<210> 1

<211> 238

<212> PRT

<213> Aequorea victoria

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Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
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Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20   25   30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35   40   45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50   55   60

Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
65   70   75   80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85   90   95

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Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
        100             105             110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115             120             125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130             135             140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145             150             155             160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
            165             170             175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
        180             185             190

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
        195             200             205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
    210             215             220

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
225             230             235
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<213> Aequorea victoria

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Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1           5           10              15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
        20              25              30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35              40              45
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Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50              55              60

Ser Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
65              70              75                          80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
            85              90                          95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100             105             110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115             120             125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130             135             140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145             150             155             160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
            165             170             175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
        180             185             190

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
        195             200             205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
    210             215             220

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
225             230             235
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<213> Aequorea victoria

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Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1   5   10   15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20   25   30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35   40   45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
        50   55   60

Ser His Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
65   70   75   80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85   90   95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100   105   110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115   120   125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130   135   140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145   150   155   160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
                165   170   175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
            180   185   190

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
        195   200   205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
        210   215   220

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Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
225             230             235
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<213> Aequorea victoria

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Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
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Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20              25              30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35              40              45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50              55              60

Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65              70              75              80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
            85              90              95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
        100             105             110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
    115             120             125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130             135             140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145             150             155             160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
            165             170             175
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```
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
            180                 185                 190


Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
            195                 200                 205


Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
    210                 215                 220


Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
225                 230                 235
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<213> Aequorea victoria

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Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
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Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30


Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45


Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60


Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80


Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95


Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110


Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
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7

```
              115                    120                    125

   Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
       130                    135                    140

   Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
   145                    150                    155                    160

   Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
                      165                    170                    175

   Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
                      180                    185                    190

   Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu
                  195                    200                    205

   Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
       210                    215                    220

   Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
   225                    230                    235
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<213> Aequorea victoria

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   Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
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   Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
                  20                    25                    30

   Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
           35                    40                    45

   Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
       50                    55                    60
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8

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Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65              70              75              80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
            85              90              95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100             105             110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115             120             125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130             135             140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145             150             155             160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
            165             170             175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
        180             185             190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu
    195             200             205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
    210             215             220

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
225             230             235
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<400>   7
cc atg gcc ggt ggt acc ggt tcc ggt gcc ctg aag aag gag ctg cag          47
   Met Ala Gly Gly Thr Gly Ser Gly Ala Leu Lys Lys Glu Leu Gln
    1               5                  10                  15

gcc aac aag aag gag ctg gcc cag ctg aag tgg gag ctg cag gcc ctg          95
Ala Asn Lys Lys Glu Leu Ala Gln Leu Lys Trp Glu Leu Gln Ala Leu
                 20                  25                  30

aag aag gag ctg gcc cag tag gatcc                                        121
Lys Lys Glu Leu Ala Gln
                 35


<210>   8

<211>   37

<212>   PRT

<213>   Human


<400>   8

Met Ala Gly Gly Thr Gly Ser Gly Ala Leu Lys Lys Glu Leu Gln Ala
 1               5                  10                  15

Asn Lys Lys Glu Leu Ala Gln Leu Lys Trp Glu Leu Gln Ala Leu Lys
                 20                  25                  30

Lys Glu Leu Ala Gln
         35


<210>   9

<211>   121

<212>   DNA

<213>   Human


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<221>   CDS
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<222>   (3)..(116)

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<400>  9
cc atg gcc agc gag cag ctg gag aag aag ctg cag gcc ctg gag aag        47
   Met Ala Ser Glu Gln Leu Glu Lys Lys Leu Gln Ala Leu Glu Lys
   1               5               10              15

aag ctg gcc cag ctg gag tgg aag aac cag gcc ctg gag aag aag ctg       95
Lys Leu Ala Gln Leu Glu Trp Lys Asn Gln Ala Leu Glu Lys Lys Leu
             20              25              30

gcc cag ggc ggc acc ggt tag gatcc                                    121
Ala Gln Gly Gly Thr Gly
         35


<210>  10

<211>  37

<212>  PRT

<213>  Human


<400>  10

Met Ala Ser Glu Gln Leu Glu Lys Lys Leu Gln Ala Leu Glu Lys Lys
1               5               10              15

Leu Ala Gln Leu Glu Trp Lys Asn Gln Ala Leu Glu Lys Lys Leu Ala
             20              25              30

Gln Gly Gly Thr Gly
         35


<210>  11

<211>  19

<212>  PRT

<213>  Human


<400>  11

Gly Ser Gly Ser Gly Ser Gly Asp Ile Thr Ser Leu Tyr Lys Lys Ala
1               5               10              15
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Gly Ser Thr

<210> 12

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<212> PRT

<213> Human

<400> 12

Gly Ser Gly Ser Gly Ser Gly Asp Ile Thr Ser Leu Tyr Lys Lys Ala
1   5   10   15

Gly Ser Thr

<210> 13

<211> 18

<212> PRT

<213> human

<400> 13

Asp Pro Ala Phe Leu Tyr Lys Val Val Ile Ser Gly Ser Gly Ser Gly
1   5   10   15

Ser Gly

<210> 14

<211> 18

<212> PRT

<213> Human

<400> 14

Asp Pro Ala Phe Leu Tyr Lys Val Val Ile Ser Gly Ser Gly Ser Gly
1   5   10   15

Ser Gly

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gtcattccag ttttagaagc tc   22

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<400>  17
cagacaatct gtgtgggcac tcgaccgg                                    28


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<400>  18
catggccggt ggtaccggtt ccggtgccct gaagaaggag ctgcagg               47


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<400> 19
agctccttct tcagggcacc ggaaccggta ccaccggc   38

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ccaacaagaa ggagctggcc cagctgaagt gggagctgca g   41

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ctcccacttc agctgggcca gctccttctt gttggcctgc   40

<210> 22

<211> 27

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<400> 22
gccctgaaga aggagctggc ccagtag   27

<210> 23

<211> 37

<212> DNA

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<400> 23
gatcctactg ggccagctcc ttcttcaggg cctgcag   37

<210> 24

<211> 40

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<400> 24
catggccagc gagcagctgg agaagaagct gcaggccctg   40

<210> 25

<211> 31

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<400> 25
cctgcagctt cttctccagc tgctcgctgg c   31

<210> 26

<211> 45

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<400> 26
gagaagaagc tggcccagct ggagtggaag aaccaggccc tggag   45

<210> 27

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<400> 27
ggcctggttc ttccactcca gctgggccag cttcttctcc aggg   44

<210> 28

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<400>  28
aagaagctgg cccagggcgg caccggttag                                        30


<210>  29

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<400>  29
gatcctaacc ggtgccgccc tgggccagct tcttctccag                             40


<210>  30

<211>  24

<212>  DNA

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<400> 30
ggcgccatgg tgagcaaggg cgag   24

<210> 31

<211> 35

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<400> 31
gccggaccgg taccaccgtt gtactccagc ttgtg   35

<210> 32

<211> 33

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<400>   32
gccggaccgg taccaccctg cttgtcggcc atg                              33


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<211>   36

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<400>   33
gccggaccgg taccaccctc gatgttgtgg cggatc                          36


<210>   34

<211>   32

<212>   DNA

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<400>   34
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<210>   35

<211>   36

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<400>   35
ggcgccatgg gcaccggtta caacagccac aacgtc                              36

<210>   36

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<212>   DNA

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<400>   36
ggcgccatgg gcaccggtaa gaacggcatc aaggtg                              36

<210>   37

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<212>   DNA
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<400> 37
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<210> 38

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<400> 38
gggggctagc gccaccatgg tgagcaaggg cgag   34

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<400>  39
gcgggggatc cgatatcgcc agagccagag ccagagccct cgatgttgtg gcggatc          57


<210>  40

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gggggctagc gatatccggc tctggctctg gctctggcga cggcagcgtg cagctc          56


<210>  41

<211>  64

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<400>  41
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catg                                                                  64


<210>  42

<211>  64

<212>  DNA

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<400>  42
catgtggtcg gggtagcggg cgaagcactg caggccgtag ccgaaggtgg tcacgagggt      60

gggc                                                                  64


<210>  43

<211>  64

<212>  DNA

<213>  Artificial Sequence


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<223>  Primer sequence

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<223>  Primer sequence


<400>  43
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gcccaccctc gtgaccaccc tgggctacgg cctgcagtgc ttcgcccgct accccgacca          60

catg                                                                       64
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<210> 44

<211> 64

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<400> 44
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catgtggtcg gggtagcggg cgaagcactg caggccgtag cccagggtgg tcacgagggt          60

gggc                                                                       64
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<210> 45

<211> 36

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<221> misc_feature

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<400> 45
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gacaaccact acctgagcta ccagtccgcc ctgagc                                    36
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<210> 46

<211> 36

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<400> 46
gctcagggcg gactggtagc tcaggtagtg gttgtc   36

<210> 47

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<400> 47
ccaccatggg agtgcaggtg gaaacc   26

<210> 48

<211> 19

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<400> 48
cttccagttt tagaagctc   19

<210> 49

<211> 29

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<400> 49
ccaccatgga gatgtggcat gaaggcctg   29

<210> 50

<211> 25

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cctgctttga gattcgtcgg aacac   25

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<400> 51
tcctaggtca gtcctgctcc tcggccacga agtgcactcc taggctgcag cacgtgttga   60

caattaatca tcgg   74

<210> 52

<211> 28

<212> DNA

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<400> 52
cagacaatct gtgtgggcac tcgaccgg   28

<210> 53

<211> 59

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<400> 53
gcgggggatc cgatatcgcc agagccagag ccagagccct gggccagctc cttcttcag   59

<210> 54

<211> 28

<212> DNA

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<400> 54
cctacttgga gctggtgtac ttggtgac   28

<210> 55

<211> 56

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<213> Artificial sequence

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<400> 55
gggggctagc gatatccggc tctggctctg gctctggcga cggcagcgtg cagctc   56

<210> 56

<211> 29

<212> DNA

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<400> 56
ccaccatggc tactcaagct gatttgatg   29

<210> 57

<211> 25

<212> DNA

<213> Artificial sequence

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<400> 57
ccaggtcagt atcaaaccag gccag   25

<210> 58

<211> 28

<212> DNA

<213> Artificial sequence

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<400> 58
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<210> 59

<211> 36

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gttgctagca ccatgcctga gccagccaag tctgct                                    36


<210>  60

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<400>  60
gttgatatcc cttggagctg gtgtacttgg tgac                                      34


<210>  61

<211>  29

<212>  DNA

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<220>

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<400>  61
ccaccatgcc gcagctgaac ggcggtgga                                            29
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<210>  62

<211>  22

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<400>  62
caggcggagg ccgtctttcc gc                                          22


<210>  63

<211>  36

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<400>  63
gttcagctga tgggagtgca ggtggaaacc atctcc                           36


<210>  64

<211>  60

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<400> 64
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<210> 65

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<400> 65
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<210> 66

<211> 35

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<210>  67

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<400>  67
ccaccatgcc tgagccagcc aagtctgct                                  29


<210>  68

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<220>
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<221>  misc_feature

<223>  Primer sequence


<400>  68
ccttggagct ggtgtacttg gtgac                                          25


<210>  69

<211>  18

<212>  PRT

<213>  Artificial sequence


<220>

<223>  Linker Sequence

<400>  69

Asp Pro Ala Phe Leu Tyr Lys Val Val Ile Ser Gly Ser Gly Ser Gly
1                   5                   10                  15

Ser Gly


<210>  70

<211>  19

<212>  PRT

<213>  Artificial sequence


<220>

<223>  Linker sequence

<400>  70

Gly Ser Gly Ser Gly Ser Gly Asp Ile Thr Ser Leu Tyr Lys Lys Ala
1                   5                   10                  15

Gly Ser Thr
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<210>  71
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<220>

<223>  Linker sequence

<400>  71

Asp Pro Ala Phe Leu Tyr Lys Val Val Ile Ser Gly Ser Gly Ser Gly
1               5               10              15


<210>  72
<211>  9
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<213>  Artificial sequence


<220>

<223>  Linker sequence

<400>  72

Gly Ser Gly Ser Gly Ser Gly Asp Leu
1               5


<210>  73
<211>  18
<212>  PRT
<213>  Artificial sequence


<220>

<223>  Linker sequence

<400>  73

Asp Pro Ala Phe Leu Tyr Lys Val Val Ile Ser Gly Thr Gly Thr Gly
1               5               10              15
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Thr Gly

<210> 74

<211> 19

<212> PRT

<213> Artificial sequence

<220>

<223> Linker sequence

<400> 74

Gly Ser Gly Ser Gly Ser Gly Asp Ile Thr Ser Leu Tyr Lys Lys Ala
1   5   10   15

Gly Ser Thr

<210> 75

<211> 12

<212> PRT

<213> Artificial sequence

<220>

<223> Linker sequence

<400> 75

Asp Ile Thr Ser Leu Tyr Lys Lys Ala Gly Ser Thr
1   5   10

<210> 76

<211> 19

<212> PRT

<213> Artificial sequence

<220>

<223> Linker sequence

<400> 76

Gly Thr Gly Thr Gly Thr Gly Asp Ile Thr Ser Leu Tyr Lys Lys Ala
1   5   10   15

Gly Ser Thr

<210> 77

<211> 10

<212> PRT

<213> Artificial sequence

<220>

<223> Linker sequence

<400> 77

Leu Pro Ser Gly Ser Gly Ser Gly Ser Gly
1   5   10